Sequence Alignments

RESULT 3
AAA95442
ID   AAA95442 standard; cDNA; 3280 BP.
XX
AC   AAA95442;
XX
DT   12-FEB-2001 (first entry)
XX
DE   Human CASB619 protein coding sequence #1.
XX
KW   Human; CASB619; cancer; autoimmune disease; immunogen; vaccine;
KW   epitope; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..3342
FT   /*tag= a
FT   /product= "CASB619"

Wed Mar 12 10:08:32 2003

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XX
PN   WO200058460-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-EP02478.
XX
PR   26-MAR-1999;  99GB-0007113.
PR   25-SEP-1999;  99GB-0022858.
XX
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Bruck CEM, Cassart J, Coche T, Vinals De Bassols YC;
XX
DR   WPI; 2000-664923/64.
DR   P-PSDB; AAB26179.
XX
PT   Novel CASB619 polypeptides useful for diagnosing, and as vaccines for
PT   prophylactic and therapeutic treatment of, cancers, particularly
PT   ovarian and colon carcinoma, and autoimmune diseases -
XX
PS   Claim 13; Page 53-54; 68pp; English.
XX
CC   The present sequence comprises the human CASB619 coding sequence. This
CC   protein is thought to be specifically or over-expressed in tumour cells,
CC   and so can be used as a target for antigen-specific immune responses
CC   which can cause destruction of the tumour cell. In addition, the protein
CC   and gene can be used in cancer diagnosis, in the treatment of autoimmune
CC   diseases and in vaccines against cancer and autoimmune disease. The
CC   invention provides a number of epitopes derived from the protein which
CC   can be used as immunogens.
XX
SQ   Sequence 3280 BP; 810 A; 930 C; 797 G; 743 T; 0 other;

Query Match       97.8%;  Score 3259.6;  DB 21;  Length 3280;
Best Local Similarity  99.8%;  Pred. No. 0;
Matches 3273;  Conservative  0;  Mismatches  4;  Indels  1;  Gaps  1;

Qy    58 ATGGCTGAGCCTGGGCACGCCAGCCCATCCTCCGCCAGTCAGGGGAAGAACTGAGAGG 117
          ||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db     1 ATGGCTGAGCCTGGGCACGCCAGCCACCATCTCTCCGCCAGTCAGGGGAAGAACTGAGAGG 60

Qy   118 CGCATACCCCGGCTGTGGCGGCTCGTGCTCGCTGCTCGCTGCTCGGGCTGGGACCCCAG 177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CGCATACCCCGGCTGTGGCGGCTCGTGCTCGCTGCTCGCTGCTCGGGCTGGGACCCCAG 120

Qy   178 GGAACGGGACCGGAGCTTCACGCGTCGCAAAGAGTCTGAGTACCACTATGAGTACACGGCG 237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAACGGGACCGGAGCTTCACGCGTCGCAAAGAGTCTGAGTACCACTATGAGTACACGGCG 180

Qy   238 TGTGACAGCAGCGGTTCCAGGTGGAGGGGTCGCCCGTGCCCGCATACCCCGGGGCCGTGCACC 297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGTGACAGCAGCGGTTCCAGGTGGAGGGGTCGCCCGTGCCCGCATACCCCGGGGCCGTGCACC 240

Qy   298 AGCCTGCCTGACCCCCGTCAAGGCACCGAGTGTCCTCCTTCCTTCTGCAAACGCCGGGGAGTTT 357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AGCCTGCCTGACCCCCGTCAAGGCACCGAGTGTCCTCCTTCCTTCTGCAAACGCCGGGGAGTTT 300

Qy   358 CTGGATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCTGAGGGCCTCCCTCGGCACA 417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCTGAGGGCCTCCCTCGGCACA 360

Qy   418 GGCATTCGGTTTGATGAGTGGGATGAGCTCCTTGCCAGCCTTCTTCGTCAGCCAAC 477
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GGCATTCGGTTTGATGAGTGGGATGAGCTCCTTGCCAGCCTTCTTCGTCAGCCAAC 420

Qy   478 ATGGAGCTGGATGACAGTGCTGCTGAGTCCACGGGAACTGTACTTCGTCCAAGTGGGTT 537
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGGAGCTGGATGACAGTGCTGCTGAGTCCACGGGAACTGTACTTCGTCCAAGTGGGTT 480

Qy   538 CCCCGGGGCGACTACATCGCCTTCAACACGGGACGAATGCAACGCCACCACTGATGTAGCGCC 597
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCCCGGGGCGACTACATCGCCTTCAACACGGGACGAATGCAACGCCACCACTGATGTAGCGCC 540

Qy   598 GTCAACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATTCCGAGACTCCAGCATC 657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GTCAACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATTCCGAGACTCCAGCATC 600

Qy   658 ATCTTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGG 717
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 ATCTTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGG 660

Qy   718 ATGAAGACCACAGAAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAAT 777
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ATGAAGACCACAGAAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAAT 720

Qy   778 GTCCTCTATTGGAGACCACAGCCTTCCAGTATGGACCAAAGTACCCAGGCCTGTGCTG 837
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GTCCTCTATTGGAGACCACAGCCTTCCAGTATGGACCAAAGTACCCAGGCCTGTGCTG 780

Qy   838 GTGAGAAACATTGCCATAAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCT 897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GTGAGAAACATTGCCATAAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCT 840

Qy   898 GGCACGTATGCACAAGCAGGCAGGGCTCCTCTTTTCTGCAAACTTTGCCCAGCCAACTCTTAT 957
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GGCACGTATGCACAAGCAGGCAGGGCTCCTCTTTTCTGCAAACTTTGCCCAGCCAACTCTTAT 900

Qy   958 TCAAATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGA 1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TCAAATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGA 960

Qy  1018 TCTTCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACG 1077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TCTTCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACG 1020

Qy  1078 GCCTGCGATGCCAACGGAGGAGCACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGT 1137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GCCTGCGATGCCAACGGAGGAGCACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGT 1080

Qy  1138 AGCGAGGACCTTGAGGGGCCAGTGAAGCTGCCTGCCTGCCTGGTGTGAAGACCCACTGCCCA 1197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 AGCGAGGACCTTGAGGGGCCAGTGAAGCTGCCTGCCTGCCTGGTGTGAAGACCCACTGCCCA 1140

Qy  1198 CCCTGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCCATATGGT 1257
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 CCCTGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCCATATGGT 1200

Qy  1258 TCCTACTCCAATGGCTCAGACTGTACCCGCGTGCCCTGCCAGGGACTGAACCTGCTGTGGGA 1317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 TCCTACTCCAATGGCTCAGACTGTACCCGCGTGCCCTGCCAGGGACTGAACCTGCTGTGGGA 1260

Qy  1318 TTTGAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGCCGTTCTCAGTGGG 1377
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 TTTGAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGCCGTTCTCAGTGGG 1320

Qy  1378 ATCAACTTCGAGTACAAGGGCATGACAGGCTGGAGTGGCTGTGATCACATTTACACA 1437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 ATCAACTTCGAGTACAAGGGCATGACAGGCTGGAGTGGCTGTGATCACATTTACACA 1380

Qy  1438 GCTGCTGGAGCCTCAGACAATGACAGTTCTCACTCTGTTGTCCAGGATTTAGA 1497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 GCTGCTGGAGCCTCAGACAATGACAGTTCTCACTCTGTTGTCCAGGATTTAGA 1440

Qy  1498 CCTCCGCAGTCGGTGATGTCTGTTCTGTGAGGCTGCCAGAATCACATTTGTC 1557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 CCTCCGCAGTCGGTGATGTCTGTTCTGTGAGGCTGCCAGAATCACATTTGTC 1500

Qy  1558 TTTGAGACCCTCGTTCTGTGAACTGTGAGCTCTCATGGTGTGAATTCTAGG 1617
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 TTTGAGACCCTCGTTCTGTGAACTGTGAGCTCTCATGGTGTGAATTCTAGG 1560

Qy  1618 ACCAACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATC 1677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 ACCAACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATC 1620
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Qy 1678 ATTGAGGAGAACTACCACGAGCTTCACCTGGCCTTCCAGAGGACCACCACTTTCATGAG 1737
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1621 ATTGAGGAGAACTACCACGAGCTTCACCTGGCCTTCCAGAGGACCACCACTTTCATGAG 1680

Qy 1738 GCAAGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTT 1797
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1681 GCAAGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTT 1740

Qy 1798 ATGAATGGCGTGGCCTCCTACTGCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCC 1857
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1741 ATGAATGGCGTGGCCTCCTACTGCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCC 1800

Qy 1858 TCCTGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCC 1917
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801 TCCTGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCC 1860

Qy 1918 TGCCCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGCCTGTGTGCCC 1977
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1861 TGCCCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGCCTGTGTGCCC 1920

Qy 1978 TGTGGTCAGGGACCAAGAACAACAACAAGATCCACCTCTCTGTGCTACAATGATTGCACCTTC 2037
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1921 TGTGGTCAGGGACCAAGAACAACAACAAGATCCACCTCTCTGTGCTACAATGATTGCACCTTC 1980

Qy 2038 TCACGCAACACTCCAACCAGGACTTTCAACTACAACTCTCCGCTTTGGCAAACACCGTC 2097
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1981 TCACGCAACACTCCAACCAGGACTTTCAACTACAACTCTCCGCTTTGGCAAACACCGTC 2040

Qy 2098 ACTCTTGCTGGAGGGCCAAGCTTCCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACC 2157
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2041 ACTCTTGCTGGAGGGCCAAGCTTCCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACC 2100

Qy 2158 CTCAGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGAC 2217
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2101 CTCAGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGAC 2160

Qy 2218 GCAGTGGATCATCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTC 2277
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2161 CTCCGGATTCCTGAGGGTGAGTCAGGGTTCTCAAATCTATCACAGCCTACGTCTGCCAG 2220

Qy 2278 GCAGTGCATCATCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTC 2337
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2221 GCAGTGCATCATCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTC 2280

Qy 2338 AGCCTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCC 2397
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2281 AGCCTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCC 2340

Qy 2398 CCAGCTGAACTTTTCCACCTGGAGTTCCTTGGAATACCGGACGTGATCTTCTTTTATAGG 2457
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2341 CCAGCTGAACTTTTCCACCTGGAGTTCCTTGGAATACCGGACGTGATCTTCTTTTATAGG 2400

Qy 2458 TCCAATGATGTGACCCAGTTCTGGGAGATCAACCATCCGCGTCAGGTGC 2517
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 2401 TCCAATGATGTGACCCAGTTCTGGGAGATCAACCATCCGCGTCAGGTGC 2460

Qy 2518 AGTCCACAGAAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACC 2577
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2461 AGTCCACAGAAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACC 2520

Qy 2578 TGTGATGGCTGCAACTTGCAACCCAAGCTGTCTCGGTGGCATTTCTTCGCTGCCTGAGAGTCACC 2637
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2521 TGTGATGGCTGCAACTTGCAACCCAAGCTGTCTCGGTGGCATTTCTTCGCTGCCTGAGAGTCACC 2580

Qy 2638 GTGGCTGACTACCAGTCCTATCGTCGCAGCGTGTGTGGCTGGCTGTGTCTGGCTGTGTCCAGAAGACTACTTAC 2697
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2581 GTGGCTGACTACCAGTCCTATCGTCGCAGCGTGTGTGGCTGGCTGTGTCTGGCTGTGTCCAGAAGACTACTTAC 2640

Qy 2698 GTGTGGCGAGAACCCAAGCTATGCCTGTCGGTGGCATTTCTTCTGCCTGAGCAGAGAGTCACC 2757
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2641 GTGTGGCGAGAACCCAAGCTATGCCTGTCGGTGGCATTTCTTCTGCCTGAGCAGAGAGTCACC 2700

Qy 2758 ATCTGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCC 2817
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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2701 ATCTGCAAAACCATAGATTTCTGCGTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCC 2760

Qy 2818 ATCCTGCTCACCGTCTTGACCTGCTCTACTTTGGAAAAGAATCAAAAACTAGAGTACAAG 2877
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2761 ATCCTGCTCACCGTCTTGACCTGCTCTACTTTGGAAAAAGAATCAAAAACTAGAGTACAAG 2820

Qy 2878 TACTCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACTGCCAGCAGCTGACAGC 2937
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2821 TACTCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACTGCCAGCAGCTGACAGC 2880

Qy 2938 TGCGGCCATCATGGAAGGCGAGGATGTAGAGGACGACCACCTCATCTTTACCAGCAAGAA-TCA 2996
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db 2881 TGCGGCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAAGTCA 2940

Qy 2997 CTCTTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTGACTCAGTG 3056
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2941 CTCTTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTGACTCAGTG 3000

Qy 3057 CCGCTGAAGACATCCTCAGGAGGCCCAGACACTGTGGACCTGTGAGAGGCACTGCCTGCCTCA 3116
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3001 CCGCTGAAGACATCCTCAGGAGGCCCAGACACTGTGGACCTGTGAGAGGCACTGCCTGCCTCA 3060

Qy 3117 CCTGCCTCCTCACCTTGCATAGCACCTGCAAGCCTGCGGCGGATTTGGGTGCCAGCATC 3176
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3061 CCTGCCTCCTCACCTTGCATAGCACCTGCAAGCCTGCGGCGGATTTGGGTGCCAGCATC 3120

Qy 3177 CTGCAACACACCCACTGCTGGAAATCTTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAG 3236
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3121 CTGCAACACACCCACTGCTGGAAATCTTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAG 3180

Qy 3237 ATCTTTTTTATAGAGTACCCAAACCCTCCTTCTGCTTGCTGCTCAAACCTGCCAAATATA 3296
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3181 ATCTTTTTTATAGAGTACCCAAACCCTCCTTCTGCTTGCTGCTCAAACCTGCCAAATATA 3240

Qy 3297 CCCACACTTTGTTGTTTGTAAATTAAAATAAAAAAAAAAAAAAA 3334
         ||||||||||||||| |||||||||||||||||||||||||||
Db 3241 CCCACACTTTGTTTGTAAAGTTTGTAAAAAAAAAAAAAAAAAAA 3278
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RESULT-2
AAB26179
ID   AAB26179 standard; Protein; 1013 AA.
XX
AC   AAB26179;
XX
DT   12-FEB-2001 (first entry)
XX
DE   Human CASB619 protein #1.
XX
KW   Human; CASB619; cancer; autoimmune disease; immunogen; vaccine;
KW   epitope.
XX
OS   Homo sapiens.
XX
PN   WO200058460-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-EP02478.
XX
PR   26-MAR-1999; 99GB-0007113.
PR   25-SEP-1999; 99GB-0022858.
XX
PA   (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Bruck CEM, Cassart J, Coche T, Vinals De Bassols YC;
XX
DR   WPI: 2000-664923/64.
DR   N-PSDB: AAA95442.
XX
PT   Novel CASB619 polypeptides useful for diagnosing, and as vaccines for
PT   prophylactic and therapeutic treatment of, cancers, particularly
PT   ovarian and colon carcinoma, and autoimmune diseases
XX
PS   Claim 4; Page 54-56; 68pp; English.
XX
CC   The present sequence comprises the human CASB619 protein sequence. This
CC   protein is thought to be specifically or over-expressed in tumour cells,
CC   and so can be used as a target for antigen-specific immune responses
CC   which can cause destruction of the tumour cell. In addition, the protein
CC   and gene can be used in cancer diagnosis, in the treatment of autoimmune
CC   diseases and in vaccines against cancer and autoimmune disease. The
CC   invention provides a number of epitopes derived from the protein which
CC   can be used as immunogens.
XX
SQ   Sequence 1013 AA;

Query Match   97.6%; Score 5376; DB 21; Length 1013;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 978; Conservative 1; Mismatches 1; Indels 5; Gaps 0;

Qy   1 MAEPGHSHHLSARVRGRTERRIPRLWRLLLWAGTAFQVTQGTGPELHACKESEYHYEYTA 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MAEPGHSHHLSARVRGRTERRIPRLWRLLLWAGTAFQVTQGTGPELHACKESEYHYEYTA 60

Qy   61 CDSTGSRWRVAVPHTPGLCTSLPDPVKGTECSFSCNAGEFLDMKDQSCKPCAEGRYSLGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CDSTGSRWRVAVPHTPGLCTSLPDPVKGTECSFSCNAGEFLDMKDQSCKPCAEGRYSLGT 120

Qy   121 GIRFDEWDELPHGFASLSANMELDDSAAESTGNCTSSKWVPRGDYIAFNTDECTATLMYA 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GIRFDEWDELPHGFASLSANMELDDSAAESTGNCTSSKWVPRGDYIASNTDECTATLMYA 180

Qy   181 VNLKQSGTVNFEYYYPDSSIIFEFFVQNDQCQPNADDSRWMKTTEKGWEFHSVELNRGNN 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VNLKQSGTVNFEYYYPDSSIIFEFFVQNDQCQPNADDSRWMKTTEKGWEFHSVELNRGNN 240

Qy   241 VLYWRTTAFSVWTKVPKPVLVRNIAITGVAYTSECFPCKPGTYADKQGSSFCKLCPANSY 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 VLYWRTTAFSVWTKVPKPVLVRNIAITGVAYTSECFPCKPGTYADKQGSSFCKLCPANSY 300

Qy   301 SNKGETSCHQCDPDKYSEKGSSSCNVRPACTDKDYFYTHTACDANGETQLMYKWAKPKIC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SNKGETSCHQCDPDKYSEKGSSSCNVRPACTDKDYFYTHTACDANGETQLMYKWAKPKIC 360

Qy   361 SEDLEGAVKLPASGVKTHCPPCNPGFFKTNNSTCQPCPYGSYSNGSDCTRCPAGTEPAVG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 SEDLEGAVKLPASGVKTHCPPCNPGFFKTNNSTCQPCPYGSYSNGSDCTRCPAGTEPAVG 420

Qy   421 FEYKWWNTLPTNMETTVLSGINFEYKGMTGWEVAGDHIYTAAGASDNDFMILTLVVPGFR 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 FEYKWWNTLPTNMETTVLSGINFEYKGMTGWEVAGDHIYTAAGASDNDFMILTLVVPGFR 480

Qy   481 PPQSVMADTENKEVARITFVFETLCSVNCELYFMVGVNSRTNTPVETWKGSKGKQSYTYI 540
           |||||||||||||||||||||||||||||||||||||+|||||||||||||||||||||
Db   481 PPQSVMADTENKEVARITFVFETLCSVNCELYFMVGVNSRTNTPVETWKGSKGKQSYTYI 540

Qy   541 IEENTTTSFTWAFQRTFHEASRKYTNDVAKIYSINVTNVMNGVASYCRPCALEASDVGS 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 IEENTTTSFTWAFQRTFHEASRKYTNDVAKIYSINVTNVMNGVASYCRPCALEASDVGS 600

Qy   601 SCTSCPAGYYIDRDSGTCHSCPPNTILKAHQPYGVQACVPCGPGTKNNKIHSLCYNDCTF 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 SCTSCPAGYYIDRDSGTCHSCPPNTILKAHQPYGVQACVPCGPGTKNNKIHSLCYNDCTF 660

Qy   661 SRNTPTRTFNYNFSALANTVTLAGGPSFTSKGLKYFHHFTLSLCGNQGRKMSVCTDNVTD 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 SRNTPTRTFNYNFSALANTVTLAGGPSFTSKGLKYFHHFTLSLCGNQGRKMSVCTDNVTD 720

Qy   721 LRIPEGESGFSKSITAYVCQAVIIPPEVTGYKAGVSSQPVSLADRLIGVTTDMTLDGITS 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 LRIPEGESGFSKSITAYVCQAVIIPPEVTGYKAGVSSQPVSLADRLIGVTTDMTLDGITS 780

Qy   781 PAELFHLESLGIPDVIFFYRSNDVTQSCSSGRSTTIRVRCSPQKTVPGSLLLPGTCSDGT 840
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Db   781 PAELFHLESLGIPDVIFFYRSNDVTQSCSSGRSTTIRVRCSPQKTVPGSLLLPGTCSDGT 840

Qy   841 CDGCNFHFLWESAAACPLCSVADYHAIVSSCVAGIQKTTYVWREPKLCSGGISLPEQRVT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CDGCNFHFLWESAAACPLCSVADYHAIVSSCVAGIQKTTYVWREPKLCSGGISLPEQRVT 900

Qy   901 ICKTIDFWLKVGISAGTCTAILLTVLTCYFWKKNQKLEYKYSKLVMNATLKDCDLPAADS 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ICKTIDFWLKVGISAGTCTAILLTVLTCYFWKKNQKLEYKYSKLVMNATLKDCDLPAADS 960

Qy   961 CAIMEGEDVEDDLIFTSKNHSLGR 984
           ||||||||||||||||||||||:
Db   961 CAIMEGEDVEDDLIFTSKKSLFGK 984

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COMPUTER:  IBM PC compatible
OPERATING SYSTEM:  PC-DOS/MS-DOS
SOFTWARE:  PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
    APPLICATION NUMBER:  US/08/190,029A
    FILING DATE:  28-FEB-1994
    CLASSIFICATION:  435
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  PCT/GB92/01389
    FILING DATE:  27-JUL-1992
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  GB 9202401.7
    FILING DATE:  05-FEB-1992
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  GB 9116325.3
    FILING DATE:  29-JUL-1991
ATTORNEY/AGENT INFORMATION:
    NAME:  JOHN J. MCDONNELL
    REGISTRATION NUMBER:  26,949
    REFERENCE/DOCKET NUMBER:  94,062
TELECOMMUNICATION INFORMATION:
    TELEPHONE:  312-715-1000
    TELEFAX:  312-715-1234
INFORMATION FOR SEQ ID NO:  10:
    SEQUENCE CHARACTERISTICS:
    LENGTH:  349 amino acids
    TYPE:  amino acid
    TOPOLOGY:  linear
    MOLECULE TYPE:  protein
US-08-190-029A-10

Query Match             100.0%;  Score  8;  DB 1;  Length 349;
Best Local Similarity   0.8%;
Matches    8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      680 VTLAGGPS 687
            ||||||||
Db      110 VTLAGGPS 117

RESULT 2
US-08-462-695-10
; Sequence 10, Application US/08462695
; Patent No. 5854025
    GENERAL INFORMATION:
    APPLICANT:  EDWARDS, Richard Mark
    APPLICANT:  BAWDEN, Lindsey
    TITLE OF INVENTION:  IGF-II ANALOGUES
    NUMBER OF SEQUENCES:  12
    CORRESPONDENCE ADDRESS:
        ADDRESSEE:  BANNER & ALLEGRETTI, LTD.
        STREET:  10 S. WACKER DRIVE, SUITE 3000
        CITY:  CHICAGO
        STATE:  ILLINOIS
        COUNTRY:  U.S.A.
        ZIP:  60606
    COMPUTER READABLE FORM:
        MEDIUM TYPE:  Floppy disk
        COMPUTER:  IBM PC compatible
        OPERATING SYSTEM:  PC-DOS/MS-DOS
        SOFTWARE:  PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER:  US/08/462,695
        FILING DATE:  5-JUN-1995
        CLASSIFICATION:  435
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER:  08/190,029
        FILING DATE:  28-FEB-1994
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER:  PCT/GB92/01389
        FILING DATE:  27-JUL-1992
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER:  GB 9202401.7
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#					Accession	Sequence
101	6	0.6	282	1	US-08-318-947A-19	Sequence 19, Appl
102	6	0.6	282	2	US-08-795-303-19	Sequence 19, Appl
103	6	0.6	282	4	US-09-071-035-222	Sequence 222, App
104	6	0.6	286	4	US-09-071-035-176	Sequence 176, App
105	6	0.6	293	4	US-09-134-001C-5333	Sequence 5333, Ap
106	6	0.6	305	4	US-09-134-001C-5038	Sequence 5038, Ap
107	6	0.6	305	4	US-09-071-035-174	Sequence 174, App
108	6	0.6	314	4	US-09-215-252-15	Sequence 15, Appl
109	6	0.6	317	4	US-08-118-270-27	Sequence 27, Appl
110	6	0.6	317	5	PCT-US93-08528-27	Sequence 27, Appl
111	6	0.6	318	4	US-09-068-051A-32	Sequence 32, Appl
112	6	0.6	324	2	US-08-793-410-30	Sequence 30, Appl
113	6	0.6	324	2	US-08-793-410-29	Sequence 29, Appl
114	6	0.6	327	1	US-07-867-105B-1	Sequence 1, Appli
115	6	0.6	328	2	US-08-651-818A-2	Sequence 2, Appli
116	6	0.6	328	2	US-08-793-410-6	Sequence 6, Appli
117	6	0.6	328	2	US-08-793-410-7	Sequence 7, Appli
118	6	0.6	328	2	US-09-184-826-2	Sequence 2, Appli
119	6	0.6	328	4	US-09-080-205-4	Sequence 4, Appli
120	6	0.6	333	2	US-08-853-659A-48	Sequence 48, Appli
121	6	0.6	341	1	US-08-356-180-4	Sequence 4, Appli
122	6	0.6	349	4	US-09-006-353A-13	Sequence 13, Appl
123	6	0.6	349	4	US-09-573-986-13	Sequence 13, Appl
124	6	0.6	350	4	US-09-157-603-1	Sequence 1, Appli
125	6	0.6	350	4	US-09-587-436-1	Sequence 1, Appli
126	6	0.6	352	4	US-08-927-165A-1	Sequence 1, Appli
127	6	0.6	352	4	US-09-576-160B-1	Sequence 1, Appli
128	6	0.6	353	1	US-08-229-418-2	Sequence 2, Appli
129	6	0.6	353	2	US-08-932-761A-2	Sequence 2, Appli
130	6	0.6	353	2	US-09-307-912-2	Sequence 2, Appli
131	6	0.6	353	5	PCT-US95-04464-2	Sequence 2, Appli
132	6	0.6	354	4	US-09-068-569-2	Sequence 2, Appli
133	6	0.6	358	4	US-09-288-143-211	Sequence 211, App
134	6	0.6	359	4	US-09-134-001C-4760	Sequence 4760, Ap
135	6	0.6	361	2	US-08-415-751-36	Sequence 36, Appli
136	6	0.6	365	4	US-08-979-424-3	Sequence 3, Appli
137	6	0.6	365	4	US-08-928-383B-2	Sequence 2, Appli
138	6	0.6	365	4	US-08-928-383B-23	Sequence 23, Appl
139	6	0.6	365	4	US-08-928-383B-24	Sequence 24, Appl
140	6	0.6	365	4	US-08-928-383B-26	Sequence 26, Appl
141	6	0.6	365	4	US-09-272-496-2	Sequence 2, Appli
142	6	0.6	366	1	US-08-554-612C-50	Sequence 50, Appl
143	6	0.6	369	1	US-08-416-756A-2	Sequence 2, Appli
144	6	0.6	369	4	US-08-880-865-2	Sequence 13, Appl
145	6	0.6	376	4	US-09-215-252-13	Sequence 23, Appl
146	6	0.6	384	2	US-08-637-759B-375	Sequence 24, Appl
147	6	0.6	384	2	US-08-871-355A-375	Sequence 375, App
148	6	0.6	384	3	US-09-201-945-375	Sequence 375, App
149	6	0.6	389	2	US-08-605-106-13	Sequence 13, Appl
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ALIGNMENTS

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RESULT 1
US-08-190-029A-10
US-08-190-029A-10, Application US/08190029A
; Sequence 10, Application US/08190029A
; Patent No. 5736363
    GENERAL INFORMATION:
    APPLICANT:  EDWARDS, Richard Mark
    APPLICANT:  BAWDEN, Lindsey
    TITLE OF INVENTION:  IGF-II ANALOGUES
    NUMBER OF SEQUENCES:  12
    CORRESPONDENCE ADDRESS:
        ADDRESSEE:  ALLEGRETTI & WITCOFF, LTD.
        STREET:  10 S. WACKER DRIVE, SUITE 3000
        CITY:  CHICAGO
        STATE:  ILLINOIS
        COUNTRY:  U.S.A.
        ZIP:  60606
    COMPUTER READABLE FORM:
        MEDIUM TYPE:  Floppy disk
    FILING DATE:
    PRIOR APPLICATION DATA:
    APPL. APP
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RESULT 1
AAF28030
ID   AAF28030 standard; DNA; 3334 BP.
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AC   AAF28030;
XX
DT   08-MAY-2001  (first entry)
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DE   Human TR13 receptor coding sequence SEQ ID NO: 39.
XX
KW   Human; tumour necrosis factor receptor; TR13; TR14; infection;
KW   cancer; autoimmune disease; allergy; inflammatory disease;
KW   graft rejection; apoptosis; cardiovascular disease; aneurysm; ds.
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OS   Homo sapiens.
XX
PN   WO200105834-A1.
XX
PD   25-JAN-2001.
XX
PF   14-JUL-2000; 2000WO-US19343.
XX
PR   16-JUL-1999;    99US-0144087.
PR   18-AUG-1999;    99US-0149450.
PR   20-AUG-1999;    99US-0149712.
PR   10-SEP-1999;    99US-0153089.
XX
PA   (HUMA-). HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ni J,  Young PE;
XX
DR   WPI; 2001-112682/12.
```

us-10-046-433-39.rng

Wed Mar, 12 10:08:32 2003

```
XX
PT   Nucleic acids encoding 2 human tumor necrosis factor receptor
PT   polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis
PT   and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT   hypohidrotic ectodermal dysplasia -
XX
PS   Claim 4; Page 394-398; 418pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   human tumour necrosis factor receptors TR13 and TR14. These sequences are
CC   useful in the diagnosis and treatment of many diseases, including cancer,
CC   autoimmune diseases, cardiovascular disorders, allergies,
CC   neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC   infections.
XX
SQ   Sequence 3334 BP; 820 A; 952 C; 811 G; 751 T; 0 other;

Query Match          100.0%;  Score 3334;  DB 22;  Length 3334;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 3334;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy         1 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACACACGCTATG 60
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Db         1 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACACACGCTATG 60

Qy        61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCCAGAGTCAGGGAGAACTGAGAGGCGC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCCAGAGTCAGGGAGAACTGAGAGGCGC 120

Qy       121 ATACCCCGGCTGTGGCGGCTGCTGCTCGGCGTGGGACCGGCCTTCCAGGTGACCCAGGGA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 ATACCCCGGCTGTGGCGGCTGCTGCTCGGCGTGGGACCGGCCTTCCAGGTGACCCAGGGA 180

Qy       181 ACGGGACCGGAGCTTCACGGCTTCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
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Db       181 ACGGGACCGGAGCTTCACGGCTTCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240

Qy       241 GACAGCACGGGTTCCAGGTGGAGGTGCGCGTGCGCCGCCATACCCGGGCCTGTGCCACCAGC 300
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Db       241 GACAGCACGGGTTCCAGGTGGAGGTGCGCGTGCGCCGCCATACCCGGGCCTGTGCCACCAGC 300

Qy       301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCGCCGGGAGTTTCTG 360
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Db       301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCGCCGGGAGTTTCTG 360

Qy       361 GATATGAAGGACCAGTCATGTCATGGGATGGGATGCTGCCCCGCTTGCCAGCCTCTCAGCACATG 420
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Db       361 GATATGAAGGACCAGTCATGTCATGGGATGGGATGCTGCCCCGCTTGCCAGCCTCTCAGCACATG 420

Qy       421 ATTCGGTTTGATGAGTGGGATGGGATGGGATGCTGCCCCCAGAGTCTGCCAGCCTTTGCTCTTT 480
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Db       421 ATTCGGTTTGATGAGTGGGATGGGATGGGATGCTGCCCCCAGAGTCTGCCAGCCTTTGCTCTTT 480

Qy       481 GAGCTGGATGACAGTGCTGCTGCTGAGTCCACCGGAACTGTACTTCGTCTCCAAGTGGGTTCCC 540
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Db       481 GAGCTGGATGACAGTGCTGCTGCTGAGTCCACCGGAACTGTACTTCGTCTCCAAGTGGGTTCCC 540

Qy       541 CGGGGCGACTACATCGCCTTCAACACGGACGGAATGGCCACAGCCACACTGATCGTACGCCGTC 600
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Db       541 CGGGGCGACTACATCGCCTTCAACACGGACGGAATGGCCACAGCCACACTGATCGTACGCCGTC 600

Qy       601 AACCTGAAGCAATCTGCACCGTTAACTTCGAATACTTCGAATCCAGACTCCAGCATCATC 660
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Db       601 AACCTGAAGCAATCTGCACCGTTAACTTCGAATACTTCGAATCCAGACTCCAGCATCATC 660

Qy       661 TTTGAGTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGCCCCAATGCAGACTCCAGGTCGATG 720
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Db       661 TTTGAGTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGCCCCAATGCAGACTCCAGGTCGATG 720

Qy       721 AAGACCACCAGAGAAAGGATGGGAATTCCACAGTGTGGAGTCAAATCAGAGGCAATAATGTC 780
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Db       721 AAGACCACCAGAGAAAGGATGGGAATTCCACAGTGTGGAGTCAAATCAGAGGCAATAATGTC 780
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Qy       781 CTCTATTGGAGAACCACCAGCCTTCTCAGTATGGACAAAGTACCCAGCCTGTGCTGGTG 840
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Db       781 CTCTATTGGAGAACCACCAGCCTTCTCAGTATGGACAAAGTACCCAGCCTGTGCTGGTG 840

Qy       841 AGAAACATTGCCATAACAGGGTGGCCTACACTTCAGAATGCTTCCCTGCAAACCTGGC 900
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Db       841 AGAAACATTGCCATAACAGGGTGGCCTACACTTCAGAATGCTTCCCTGCAAACCTGGC 900

Qy       901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 960
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Db       901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 960

Qy       961 AATAAAGGAGAAACTTCTTGCCACCAGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020
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Db       961 AATAAAGGAGAAACTTCTTGCCACCAGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020

Qy      1021 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAGAAGATTATTCTACACACACGGCC 1080
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Db      1021 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAGAAGATTATTCTACACACACGGCC 1080

Qy      1081 TGGGATGCCAACGAGAGACAACTCATGTACAAATGGCCAAGCCGAAAATCTGTAGC 1140
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Db      1081 TGGGATGCCAACGAGAGACAACTCATGTACAAATGGCCAAGCCGAAAATCTGTAGC 1140

Qy      1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTCGCCTGTGGTGTGAAGACCCACCTGCCACCC 1200
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Db      1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTCGCCTGTGGTGTGAAGACCCACCTGCCACCC 1200

Qy      1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260

Qy      1261 TACTCCAATGGCTCAGACTGTACCCCTGCCCAGGACTACACGGCGTGTGGGATTT 1320
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Db      1261 TACTCCAATGGCTCAGACTGTACCCCTGCCCAGGACTACACGGCGTGTGGGATTT 1320

Qy      1321 GAATACAAATGGAACACGTGCCCACAAACATGGAAACGACCGTTCAGTGGGATC 1380
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Db      1321 GAATACAAATGGAACACGTGCCCACAAACATGGAAACGACCGTTCAGTGGGATC 1380

Qy      1381 AACTTCGAGTACAAGGCATGGAGGTGGCTGGTGATCACATTACACAGCT 1440
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Db      1381 AACTTCGAGTACAAGGCATGGAGGTGGCTGGTGATCACATTACACAGCT 1440

Qy      1441 GCTGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCGCAGGATTTAGACCT 1500
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Db      1441 GCTGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCGCAGGATTTAGACCT 1500

Qy      1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
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Db      1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560

Qy      1561 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGTGAATTCTAGGACC 1620
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Qy      1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680
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Qy      1681 GAGGAGAACACTACCACCAGCTTCACCTGGGCCTTCACCCTGGGCCTTTCATGAGGCA 1740
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Db      1741 AGCAGGAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800

Qy      1801 AATGGCGTGGCCTCCCTACTGCCCGTCCCTGTGATGTGGGCTCCTCC 1860
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Db      1801 AATGGCGTGGCCTCCCTACTGCCCGTCCCTGTGATGTGGGCTCCTCC 1860

Qy      1861 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
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Wed Mar 12 10:08:32 2003

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Db        ||||||||||||||||||||||||||||||||||||||||||||||||||
    1861  TGCACCTCCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC  1920

Qy  1921  CCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGCCCCTGT     1980
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Db  1921  CCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGCCCCTGT     1980

Qy  1981  GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGCTACAATGATTGCACCTTCTCA     2040
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Db  1981  GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGCTACAATGATTGCACCTTCTCA     2040

Qy  2041  CGCAACACTCCAACCAGGACTTCAACTACAACTTCTCCGCTTGGCAAACACCGTCACT     2100
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Db  2041  CGCAACACTCCAACCAGGACTTCAACTACAACTTCTCCGCTTGGCAAACACCGTCACT     2100

Qy  2101  CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGTTGAAAATACTTCCATCACTTTACCCTC  2160
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Db  2101  CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGTTGAAAATACTTCCATCACTTTACCCTC  2160

Qy  2161  AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC  2220

Qy  2221  CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACCAGCCTACGTCTGCCAGGCA  2280
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Db  2221  CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACCAGCCTACGTCTGCCAGGCA  2280

Qy  2281  GTCATCATCCCCCCAGAGGTACAAGGCCGGGTTCCTCACAGCCTGTCAGC             2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  GTCATCATCCCCCCAGAGGTACAAGGCCGGGTTCCTCACAGCCTGTCAGC             2340

Qy  2341  CTTGCTGATCGACTTATTGGGTGACACAGATATGACTCCGACTGAATCACCTCCCCA      2400
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Db  2341  CTTGCTGATCGACTTATTGGGTGACACAGATATGACTCCGACTGAATCACCTCCCCA      2400

Qy  2401  GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGACGTGATCTTCTTTTATAGGTCC    2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGACGTGATCTTCTTTTATAGGTCC    2460

Qy  2461  AATGATGTGACCCAGTTCTGACCAGATCAACCACCATCCGCGTCAGGTGCAGT         2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  AATGATGTGACCCAGTTCTGACCAGATCAACCACCATCCGCGTCAGGTGCAGT         2520

Qy  2521  CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAAGTGCTCAGATGGGACCTGT  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAAGTGCTCAGATGGGACCTGT  2580

Qy  2581  GATGGGCTGCAACTTCCACTTCCTGCGTGGGAGAGCGGCGGCGTGCTTGCCCGCTCGTCAGTG  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  GATGGGCTGCAACTTCCACTTCCTGCGTGGGAGAGCGGCGGCGTGCTTGCCCGCTCGTCAGTG  2640

Qy  2641  GCTGACTACCATGCTATCGTCAGCAGCTGTGTGTGGCTGGATCCAGAGACTACTTACGTG  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GCTGACTACCATGCTATCGTCAGCAGCTGTGTGTGGCTGGATCCAGAGACTACTTACGTG  2700

Qy  2701  TGGCGGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGGCACCCATC     2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  TGGCGGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGGCACCCATC     2760

Qy  2761  TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC   2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC   2820

Qy  2821  CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAGAATCAAAAACTAGAGTACAAGTAC    2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAGAATCAAAAACTAGAGTACAAGTAC    2880

Qy  2881  TCCAAGCTGGTGATGAATGCTACTCTCCAAGGACTGTGACCTGCCAGGCTGACAGCTGC     2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  TCCAAGCTGGTGATGAATGCTACTCTCCAAGGACTGTGACCTGCCAGGCTGACAGCTGC     2940

Qy  2941  GCCATCATGGAAGGCGAGGATGTAGAGGACGACACCTCATCTTTACCAGCAAGAATCACTCT  3000
          |||||||||||||||||||||
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Db  2941  GCCATCATGGAAGGCGAGGATGTAGAGGACGACACCTCATCTTTACCAGCAAGAATCACTCT  3000

Qy  3001  TTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCGC  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  TTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCGC  3060

Qy  3061  TGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCCACCTG  3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  TGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCCACCTG  3120

Qy  3121  CCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTGGGTGCCAGCATCCTGC   3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  CCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTGGGTGCCAGCATCCTGC   3180

Qy  3181  AACACCCACTGCTGAAATCTTCATTGTGGCCTTATCAGATGTTTGAATTCAGATCT      3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  AACACCCACTGCTGAAATCTTCATTGTGGCCTTATCAGATGTTTGAATTCAGATCT      3240

Qy  3241  TTTTTTATAGAGTACCCAAACCTCCTTCTGCTTGCCTCAAACCTGCCAAATATACCCA     3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  TTTTTTATAGAGTACCCAAACCTCCTTCTGCTTGCCTCAAACCTGCCAAATATACCCA     3300

Qy  3301  CACTTTGTTTGTAAATTAAAAAAAAAAAAAAA  3334
          ||||||||||||||||||||||||||||||||
Db  3301  CACTTTGTTTGTAAATTAAAAAAAAAAAAAAA  3334
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AAB35333
ID   AAB35333 standard; Protein; 1001 AA.
XX
AC   AAB35333;
XX
DT   08-MAY-2001 (first entry)
XX
DE   Human TR13 receptor protein SEQ ID NO: 40.
XX
KW   Human; tumour necrosis factor receptor; TR13; TR14; infection;
KW   cancer; autoimmune disease; allergy; inflammatory disease;
KW   graft rejection; apoptosis; cardiovascular disease; aneurysm.
XX
OS   Homo sapiens.
XX
PN   WO200105834-A1.
XX
PD   25-JAN-2001.
XX
PF   14-JUL-2000; 2000WO-US19343.
XX
PR   16-JUL-1999;    99US-0144087.
PR   18-AUG-1999;    99US-0149450.
PR   20-AUG-1999;    99US-0149712.
PR   10-SEP-1999;    99US-0153089.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Ni J, Young PE;
XX
DR   WPI; 2001-112682/12.
XX
PT   Nucleic acids encoding 2 human tumor necrosis factor receptor
PT   polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis
PT   and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT   hypohidrotic ectodermal dysplasia -
XX
PS   Claim 40; Page 398-401; 418pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   human tumour necrosis factor receptors TR13 and TR14. These sequences are
CC   useful in the diagnosis and treatment of many diseases, including cancer,
CC   autoimmune diseases, cardiovascular disorders, allergies,
CC   neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC   infections.
XX
SQ   Sequence   1001 AA;

Query Match             100.0%;    Score 1001;  DB 22;  Length 1001;
Best Local Similarity   100.0%;    Pred. No. 0;
Matches 1001;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1 MAEPGHSHHLSARVRGRTERRIPRLWRLLLWAGTAFQVTCGTGPELHACKESEYHYEYTA 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MAEPGHSHHLSARVRGRTERRIPRLWRLLLWAGTAFQVTCGTGPELHACKESEYHYEYTA 60

Qy    61 CDSTGSRWRVAVPHTPGLCTSLPDPVKGTECSFSCNAGEFLDMKDQSCKPCAEGRYSLGT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CDSTGSRWRVAVPHTPGLCTSLPDPVKGTECSFSCNAGEFLDMKDQSCKPCAEGRYSLGT 120

Qy   121 GIRPDEWDELPHGFASLSANMELDDSAAESTGNCTSSKWVPRGDYIAFNTDECTATLMYA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GIRPDEWDELPHGFASLSANMELDDSAAESTGNCTSSKWVPRGDYIAFNTDECTATLMYA 180

Qy   181 VNLKQSGTVNFEYYYPDSSIIFEFFVONDQCOPNADDSRWMKTTEKGWEFHSVELNRGNN 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VNLKQSGTVNFEYYYPDSSIIFEFFVONDQCOPNADDSRWMKTTEKGWEFHSVELNRGNN 240

Qy   241 VLYWRTTAFSVWTKVPKPVLVRNIAITGVAYTSECFPCKPGTYADKQGSSFPCKLCPANSY 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 VLYWRTTAFSVWTKVPKPVLVRNIAITGVAYTSECFPCKPGTYADKQGSSFPCKLCPANSY 300

Qy   301 SNKGETSCHQCDPDKYSEKGSSSCNVRPACTDKDYFYTHTACDANGETQLMYKWAKPKIC 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SNKGETSCHQCDPDKYSEKGSSSCNVRPACTDKDYFYTHTACDANGETQLMYKWAKPKIC 360

Qy   361 SEDLEGAVKLPASGVKTHCPPCNPGPFKTNNSTCQPCPYGSYSNGSDCTRCPAGTEPAVG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 SEDLEGAVKLPASGVKTHCPPCNPGPFKTNNSTCQPCPYGSYSNGSDCTRCPAGTEPAVG 420

Qy   421 FEYKWWNTLPTNMETTVLSGINFEYKGMTGWEVAGDHIYTAAGASDNDFMILTLVVPGFR 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 FEYKWWNTLPTNMETTVLSGINFEYKGMTGWEVAGDHIYTAAGASDNDFMILTLVVPGFR 480

Qy   481 PPQSVWADTENKEVARITPVFETLCSVNCELYFMVGVNSRINTPVETWKGSKGKQSYTYI 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 PPQSVWADTENKEVARITPVFETLCSVNCELYFMVGVNSRINTPVETWKGSKGKQSYTYI 540

Qy   541 IEENTTTSFTWAFQRTTFHEASRKYTNDVAKIYSINVTNVMGVASYCRPCALEASDVGS 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 IEENTTTSFTWAFQRTTFHEASRKYTNDVAKIYSINVTNVMGVASYCRPCALEASDVGS 600

Qy   601 SCTSCPAGYYIDRDSGTCHSCPPNTILKAHQPYGVQACVPCGPGTKNNKIHSLCYNDCTF 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 SCTSCPAGYYIDRDSGTCHSCPPNTILKAHQPYGVQACVPCGPGTKNNKIHSLCYNDCTF 660

Qy   661 SRNTPTRTFNYNFSALANTVTLAGGPSFTSKGLKYFHHFTLSLCGNQGRKMSVCTDNVTD 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 SRNTPTRTFNYNFSALANTVTLAGGPSFTSKGLKYFHHFTLSLCGNQGRKMSVCTDNVTD 720

Qy   721 LRIPEGESGFSKSITAYVCQAVIIPPEVTGYKAGVSSQPVSLADRLIGVTTDMTLDGITS 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 LRIPEGESGFSKSITAYVCQAVIIPPEVTGYKAGVSSQPVSLADRLIGVTTDMTLDGITS 780

Qy   781 PAELFHLBSLGIPDVIFPYRSNDVTQSCSSGRSTIRVRCSPQKTVPGSLLLPGTCSDGT 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 PAELFHLBSLGIPDVIFPYRSNDVTQSCSSGRSTIRVRCSPQKTVPGSLLLPGTCSDGT 840

Qy   841 CDGCNFHFLWESAAACPLCSVADYHAIVSSCVAGIQKTTYVWREPKLCSGGISLPEQRVT 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CDGCNFHFLWESAAACPLCSVADYHAIVSSCVAGIQKTTYVWREPKLCSGGISLPEQRVT 900

Qy   901 ICKTYDFWLKVGISAGTCTAILLVLTCYFWKKNQKLEYKYSKLVMNATLKDCDLPAADS 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ICKTYDFWLKVGISAGTCTAILLVLTCYFWKKNQKLEYKYSKLVMNATLKDCDLPAADS 960

Qy   961 CAIMEGEDVEDDLLFTSKNHSLGRSNHLPPRGLLMDLTQCR 1001
          |||||||||||||||||||||||||||||||||||||||||
Db   961 CAIMEGEDVEDDLLFTSKNHSLGRSNHLPPRGLLMDLTQCR 1001
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